



#6

## SEQUENCE LISTING

&lt;110&gt; Sacktor, Todd C.

&lt;120&gt; A MEMORY ENHANCING PROTEIN

&lt;130&gt; The Research Foundation Albany

&lt;140&gt; 09/839,073

&lt;141&gt; 2001-04-20

&lt;160&gt; 4

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 2058

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (444)..(1670)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (522)

&lt;223&gt; r at position 522 is g or a

&lt;400&gt; 1

cccgccctg gagacatgag gaggcaggga tgtgaggggc gggggacagg acagccggcc 60

ttccgttaaa tatctgctcc tcgcgctcga gcctccctgc ctattgtcgg ggccggagcg 120

aagccgacgc agcatcagct cgtcaacggg aaggaagatg cctccctgca cgcccggcgc 180

gcacagagca taaagaatct gcgctgagga ggcaggagaa gaaagccgaa tctatctacc 240

gccggggagc cagaagatgg aggaagctgt accgtgccaa cggccacctc ttccaagcca 300

agcgcttaa caggagagcg tactgcggtc agtgcagcga gaggatatgg ggcctcgca 360

ggcaaggcta caggtgcata aactgcaaac tgctggtcca taagcgctgc cacggcctcg 420

tcccgtgac ctgcaggaag cat atg gat tct gtc atg cct tcc caa gag cct 473

Met Asp Ser Val Met Pro Ser Gln Glu Pro  
1 5 10cca gta gac gac aag aac gag gac gcc gac ctt cct tcc gag gag aca 521  
Pro Val Asp Asp Lys Asn Glu Asp Ala Asp Leu Pro Ser Glu Glu Thr  
15 20 25rat gga att gct tac att tcc tca tcc cgg aag cat gac agc att aaa 569  
Xaa Gly Ile Ala Tyr Ile Ser Ser Arg Lys His Asp Ser Ile Lys  
30 35 40gac gac tcg gag gac ctt aag cca gtt atc gat ggg atg gat gga atc 617  
Asp Asp Ser Glu Asp Leu Lys Pro Val Ile Asp Gly Met Asp Gly Ile  
45 50 55aaa atc tct cag ggg ctt ggg ctg cag gac ttt gac cta atc aga gtc 665  
Lys Ile Ser Gln Gly Leu Gly Leu Gln Asp Phe Asp Leu Ile Arg Val  
60 65 70

atc ggg cgc ggg agc tac gcc aag gtt ctc ctg gtg cggtt aag aag Ile Gly Arg Gly Ser Tyr Ala Lys Val Leu Leu Val Arg Leu Lys Lys 75 80 85 90	713
aat gac caa att tac gcc atg aaa gtgtgt aag aaa gag ctgtgtcat Asn Asp Gln Ile Tyr Ala Met Lys Val Val Lys Lys Glu Leu Val His 95 100 105	761
gat gac gag gat att gac tgg gta cag aca gag aag cac gtgtttt gag Asp Asp Glu Asp Ile Asp Trp Val Gln Thr Glu Lys His Val Phe Glu 110 115 120	809
cag gca tcc agc aac ccc ttc ctgtgtc gga tta cac tcc tgc ttccag Gln Ala Ser Ser Asn Pro Phe Leu Val Gly Leu His Ser Cys Phe Gln 125 130 135	857
acg aca agt cgg ttgttctgtgtcatt gag tac gtc aac ggc ggg gac Thr Thr Ser Arg Leu Phe Leu Val Ile Glu Tyr Val Asn Gly Gly Asp 140 145 150	905
ctg atg ttc cac atg cag agg cag agg aag ctc cct gag gag cac gcc Leu Met Phe His Met Gln Arg Gln Arg Lys Leu Pro Glu Glu His Ala 155 160 165 170	953
agg ttc tac gcggcc gag atc tgc atc gcc ctc aac ttctgtcac gag Arg Phe Tyr Ala Ala Glu Ile Cys Ile Ala Leu Asn Phe Leu His Glu 175 180 185	1001
agg ggg atc atc tac agg gac ctg aag ctg gac aac gtc ctc ctgtat Arg Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu Leu Asp 190 195 200	1049
gcg gac ggg cac atc aag ctc aca gac tac ggc atgtgc aag gaa ggc Ala Asp Gly His Ile Lys Leu Thr Asp Tyr Gly Met Cys Lys Glu Gly 205 210 215	1097
ctg ggc cct ggt gac aca acg agc act ttctgc gga acc ccg aat tac Leu Gly Pro Gly Asp Thr Thr Ser Thr Phe Cys Gly Thr Pro Asn Tyr 220 225 230	1145
atc gcc ccc gaa atc ctg cgg gga gag gag tac ggg ttc agc gtgtac Ile Ala Pro Glu Ile Leu Arg Gly Glu Glu Tyr Gly Phe Ser Val Asp 235 240 245 250	1193
tgg tgg gcgcgtggatcctcactgttttggatgtatggccggcgcc tcc Trp Trp Ala Leu Gly Val Leu Met Phe Glu Met Met Ala Gly Arg Ser 255 260 265	1241
ccg ttc gac atc atc acc gac aac ccg gac atg aac aca gag gac tac Pro Phe Asp Ile Ile Thr Asp Asn Pro Asp Met Asn Thr Glu Asp Tyr 270 275 280	1289
ctt ttc caa gtg atc ctg gag aag ccc atc cgg atc ccc cgg ttc ctg Leu Phe Gln Val Ile Leu Glu Lys Pro Ile Arg Ile Pro Arg Phe Leu 285 290 295	1337
tcc gtc aaa gcc tcc cat gtt tta aaa gga ttt tta aat aag gac ccc Ser Val Lys Ala Ser His Val Leu Lys Gly Phe Leu Asn Lys Asp Pro 300 305 310	1385
aaa gag agg ctc ggc tgc cgg cca cag act gga ttt tct gac atc aag Lys Glu Arg Leu Gly Cys Arg Pro Gln Thr Gly Phe Ser Asp Ile Lys 315 320 325 330	1433

tcc cac gcg ttc ttc cgc agc ata gac tgg gac ttg ctg gag aag aag	1481
Ser His Ala Phe Phe Arg Ser Ile Asp Trp Asp Leu Leu Glu Lys Lys	
335 340 345	
cag gcg ctc cct cca ttc cag cca cag atc aca gac gac tac ggt ctg	1529
Gln Ala Leu Pro Pro Phe Gln Pro Gln Ile Thr Asp Asp Tyr Gly Leu	
350 355 360	
gac aac ttt gac aca cag ttc acc agc gag ccc gtg cag ctg acc cca	1577
Asp Asn Phe Asp Thr Gln Phe Thr Ser Glu Pro Val Gln Leu Thr Pro	
365 370 375	
gac gat gag gat gcc ata aag agg atc gac cag tca gag ttc gaa ggc	1625
Asp Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser Glu Phe Glu Gly	
380 385 390	
ttt gag tat atc aac cca tta ttg ctg tcc acc gag gag tcg gtg	1670
Phe Glu Tyr Ile Asn Pro Leu Leu Leu Ser Thr Glu Glu Ser Val	
395 400 405	
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<210> 2  
<211> 409  
<212> PRT  
<213> Homo sapiens

<220>  
<221> unsure  
<222> (27)  
<223> Xaa at position 27 is Asp or Asn

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35 40 45	
Lys Pro Val Ile Asp Gly Met Asp Gly Ile Lys Ile Ser Gln Gly Leu	
50 55 60	
Gly Leu Gln Asp Phe Asp Leu Ile Arg Val Ile Gly Arg Gly Ser Tyr	
65 70 75 80	
Ala Lys Val Leu Leu Val Arg Leu Lys Lys Asn Asp Gln Ile Tyr Ala	
85 90 95	

Met Lys Val Val Lys Lys Glu Leu Val His Asp Asp Glu Asp Ile Asp  
100 105 110

Trp Val Gln Thr Glu Lys His Val Phe Glu Gln Ala Ser Ser Asn Pro  
115 120 125

Phe Leu Val Gly Leu His Ser Cys Phe Gln Thr Thr Ser Arg Leu Phe  
130 135 140

Leu Val Ile Glu Tyr Val Asn Gly Gly Asp Leu Met Phe His Met Gln  
145 150 155 160

Arg Gln Arg Lys Leu Pro Glu Glu His Ala Arg Phe Tyr Ala Ala Glu  
165 170 175

Ile Cys Ile Ala Leu Asn Phe Leu His Glu Arg Gly Ile Ile Tyr Arg  
180 185 190

Asp Leu Lys Leu Asp Asn Val Leu Leu Asp Ala Asp Gly His Ile Lys  
195 200 205

Leu Thr Asp Tyr Gly Met Cys Lys Glu Gly Leu Gly Pro Gly Asp Thr  
210 215 220

Thr Ser Thr Phe Cys Gly Thr Pro Asn Tyr Ile Ala Pro Glu Ile Leu  
225 230 235 240

Arg Gly Glu Glu Tyr Gly Phe Ser Val Asp Trp Trp Ala Leu Gly Val  
245 250 255

Leu Met Phe Glu Met Met Ala Gly Arg Ser Pro Phe Asp Ile Ile Thr  
260 265 270

Asp Asn Pro Asp Met Asn Thr Glu Asp Tyr Leu Phe Gln Val Ile Leu  
275 280 285

Glu Lys Pro Ile Arg Ile Pro Arg Phe Leu Ser Val Lys Ala Ser His  
290 295 300

Val Leu Lys Gly Phe Leu Asn Lys Asp Pro Lys Glu Arg Leu Gly Cys  
305 310 315 320

Arg Pro Gln Thr Gly Phe Ser Asp Ile Lys Ser His Ala Phe Phe Arg  
325 330 335

Ser Ile Asp Trp Asp Leu Leu Glu Lys Lys Gln Ala Leu Pro Pro Phe  
340 345 350

Gln Pro Gln Ile Thr Asp Asp Tyr Gly Leu Asp Asn Phe Asp Thr Gln  
355 360 365

Phe Thr Ser Glu Pro Val Gln Leu Thr Pro Asp Asp Glu Asp Ala Ile  
370 375 380

Lys Arg Ile Asp Gln Ser Glu Phe Glu Gly Phe Glu Tyr Ile Asn Pro  
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Leu Leu Leu Ser Thr Glu Glu Ser Val  
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<210> 3  
<211> 2058

<212> DNA  
<213> Homo sapiens

<400> 3

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ttcggctgcg tcgtactcgat gcagggtccc ttcccttac ggagggacgt gcgggcggcg 180  
cgtgtctcgat atttcttaga cgccactctt ccgtccctt ctttcggctt agatagatgg 240  
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agctacgtga ctggacgagg cgggtcccttc actcgacat cgcaggactc cttattttac 2040  
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<210> 4

<211> 13

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: mzip peptide

<400> 4

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